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C. Frank Bennett

Kenneth W. Dobie

ISIS Pharmaceuticals Inc.

<120> ANTISENSE MODULATION OF EXTRACELLULAR-SIGNAL-REGULATED KINASE-6
EXPRESSION

<130> PTS-0055WO

<150> 10/348,431

<151> 2003-01-17

<150> 10/174,465

<151> 2002-06-17

<160> 233

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cgc gcc gtg tac cgg gac ctg cag ccc gtg ggc tcg ggc gcc tac ggc																150
Arg Ala Val Tyr Arg Asp Leu Gln Pro Val Gly Ser Gly Ala Tyr Gly																
25				30				35								
gcg gtg tgc tcg gcc gtg gac ggc cgc acc ggc gct aag gtt gcc atc																198
Ala Val Cys Ser Ala Val Asp Gly Arg Thr Gly Ala Lys Val Ala Ile																
40				45				50				55				
aag aag ctg tat cgg ccc ttc cag tcc gag ctg ttc gcc aag ctc gcc																246
Lys Lys Leu Tyr Arg Pro Phe Gln Ser Glu Leu Phe Ala Lys Leu Ala																
				60				65				70				
tac cgc gag ctg cgc ctg ctc aag cac atg cgc cac gag aac gtg atc																294
Tyr Arg Glu Leu Arg Leu Leu Lys His Met Arg His Glu Asn Val Ile																
				75				80				85				
ggg ctg ctg gac gta ttc act cct gat gag acc ctg gat gac ttc acg																342
Gly Leu Leu Asp Val Phe Thr Pro Asp Glu Thr Leu Asp Asp Phe Thr																
90				95				100								
gac ttt tac ctg gtg atg ccg ttc atg ggc acc gac ctg ggc aag ctc																390
Asp Phe Tyr Leu Val Met Pro Phe Met Gly Thr Asp Leu Gly Lys Leu																
105				110				115								
atg aaa cat gag aag cta ggc gag gac cgg atc cag ttc ctc gtg tac																438
Met Lys His Glu Lys Leu Gly Glu Asp Arg Ile Gln Phe Leu Val Tyr																
120				125				130				135				
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Gln Met Met Lys Gly Leu Arg Tyr Ile His Ala Ala Gly Ile Ile His																
				140				145				150				
aga gac ctg aag ccc ggc aac ctg gct gtg aac gaa gac tgt gag ctg																534
Arg Asp Leu Lys Pro Gly Asn Leu Ala Val Asn Glu Asp Cys Glu Leu																
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 Lys Ile Leu Asp Phe Gly Leu Ala Arg Gln Ala Asp Ser Glu Met Thr
 170 175 180

ggg tac gtg gtg acc cgg tgg tac cgg gct ccc gag gtc atc ttg aat 630
 Gly Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Val Ile Leu Asn
 185 190 195

tgg atc gcg tac acg cag acg gtg gac atc tgg tct gtg ggc tgc atc 678
 Trp Ile Ala Tyr Thr Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile
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 Met Ala Glu Met Ile Thr Gly Lys Thr Leu Phe Lys Gly Ser Asp His
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 Leu Asp Gln Leu Lys Glu Ile Met Lys Val Thr Gly Thr Pro Pro Ala
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 Gly Leu Pro Glu Leu Glu Lys Lys Asp Phe Ala Ser Ile Leu Thr Asn
 265 270 275

gca agc cct ctg gct gtg aac ctc ctg gag aag atg ctg gtg ctg gac 918
 Ala Ser Pro Leu Ala Val Asn Leu Leu Glu Lys Met Leu Val Leu Asp
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 Ala Asp Ile Arg Leu Thr Ala Gly Glu Phe Leu Ser His Pro Tyr Phe
 300 305 310

gag tcc ctg cac gac acg gaa gat gag ccc cag gtc cag aag tat gat 1014

Glu Ser Leu His Asp Thr Glu Asp Glu Pro Gln Val Gln Lys Tyr Asp
315 320 325

gac tcc ttt gac tac ttt gac cgc aca ctg gat gaa tgg aag cgt gtt 1062
Asp Ser Phe Asp Tyr Phe Asp Arg Thr Leu Asp Glu Trp Lys Arg Val
330 335 340

act tac aaa gag gtg ctc agc ttc aag cct ccc cgg cag ctg ggg gcc 1110
Thr Tyr Lys Glu Val Leu Ser Phe Lys Pro Pro Arg Gln Leu Gly Ala
345 350 355

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Arg Val Ser Lys Glu Thr Pro Leu
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tggctggggc ttgcatccca aggcattcat cagagcagac gcccggttc catggacct 1277

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agggacatcc cctctcctgg gcgacgtcag tggaccttcc tgcaccccca gcctggaatg 1577

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ggggccgggt cgctagccaa gccgtccgcc ccgcagctct gcagtagaca gccgcactgg 420

caacaagggtg gccatcaaga agttgtaccg gcccttcag tcggagctgt ttgccaagcg 480

cgcctacaga gaggttgcgc tctcaaaca c atg cgc cac gag aac gtc att 532

Met Arg His Glu Asn Val Ile

1

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ggg cta ctg gat gtg ttc aca cct gat gag tct ctg gac gac ttc aca 580

Gly Leu Leu Asp Val Phe Thr Pro Asp Glu Ser Leu Asp Asp Phe Thr

10

15

20

gac ttc tac ctg gtg atg cca ttc atg ggc act gat ctg ggc aaa ctc 628

Asp Phe Tyr Leu Val Met Pro Phe Met Gly Thr Asp Leu Gly Lys Leu	
25 30 35	
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Met Lys His Glu Thr Leu Ser Glu Asp Arg Ile Gln Phe Leu Val Tyr	
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cag atg ttg aag ggg ctg aag tat atc cat gcg gct ggt gtc atc cac	724
Gln Met Leu Lys Gly Leu Lys Tyr Ile His Ala Ala Gly Val Ile His	
60 65 70	
aga gac ttg aag cct ggc aac ctg gct gtg aat gag gac tgt gag ctg	772
Arg Asp Leu Lys Pro Gly Asn Leu Ala Val Asn Glu Asp Cys Glu Leu	
75 80 85	
aag atc cta gac ttt ggc ctt gcc agg cag gca gac agt gag atg aca	820
Lys Ile Leu Asp Phe Gly Leu Ala Arg Gln Ala Asp Ser Glu Met Thr	
90 95 100	
gga tat gtg gta acc cgg tgg tat cgg gca cca gag gtc atc ttg aat	868
Gly Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Val Ile Leu Asn	
105 110 115	
tgg atg cgc tac acg cag aca gtg gac att tgg tcc gtt ggc tgc atc	916
Trp Met Arg Tyr Thr Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile	
120 125 130 135	
atg gcg gag atg att act ggg aag atc ctg ttc aaa ggc aat gac cac	964
Met Ala Glu Met Ile Thr Gly Lys Ile Leu Phe Lys Gly Asn Asp His	
140 145 150	
ctg gac cag ctg aag gag atc atg aag atc aca ggg acg ccc cct cct	1012
Leu Asp Gln Leu Lys Glu Ile Met Lys Ile Thr Gly Thr Pro Pro Pro	
155 160 165	
gag ttt gtt cag aag cta cag agt gca gag gcc aag aac tac atg gaa	1060
Glu Phe Val Gln Lys Leu Gln Ser Ala Glu Ala Lys Asn Tyr Met Glu	
170 175 180	

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 gcccctgac ccgggtccgg tcctggggcg cgtgctccg gctgggg atg agc tcc 176
 Met Ser Ser
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ccg cca ccc gcc cgc aag ggc ttt tac cgc cag gag gtg acc aaa acg 224
 Pro Pro Pro Ala Arg Lys Gly Phe Tyr Arg Gln Glu Val Thr Lys Thr
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gcc tgg gag gtg cgc gcc gtg tac caa gac ctg cag ccc gtt ggc tct 272
 Ala Trp Glu Val Arg Ala Val Tyr Gln Asp Leu Gln Pro Val Gly Ser
 20 25 30 35

ggc gcc tat ggt gca gtg tgc tct gca gta gac agc cgc act ggc aac 320

ggc ctc cct gag tta gaa aag aag gat ttt gcc tct gtc ctg acc aac 1108
 Gly Leu Pro Glu Leu Glu Lys Lys Asp Phe Ala Ser Val Leu Thr Asn
 185 190 195

gca agc cct cag gct gtg aat ctc ctg gaa agg atg ctg gtg ctg gat 1156
 Ala Ser Pro Gln Ala Val Asn Leu Leu Glu Arg Met Leu Val Leu Asp
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gcg gaa cag cgg gtg aca gca gct gag gcg tta acc cat cca tac ttt 1204
 Ala Glu Gln Arg Val Thr Ala Ala Glu Ala Leu Thr His Pro Tyr Phe
 220 225 230

gag tcc ctt cgg gac act gag gat gaa ccc aag gcc cag aaa tat gac 1252
 Glu Ser Leu Arg Asp Thr Glu Asp Glu Pro Lys Ala Gln Lys Tyr Asp
 235 240 245

gac tcc ttt gat gat gta gac cgc acc ctt gag gaa tgg aag cgt gtg 1300
 Asp Ser Phe Asp Asp Val Asp Arg Thr Leu Glu Glu Trp Lys Arg Val
 250 255 260

act tac aag gaa gtt ctc agc ttc aag cct cct agg cag cta gga gcc 1348
 Thr Tyr Lys Glu Val Leu Ser Phe Lys Pro Pro Arg Gln Leu Gly Ala
 265 270 275

aga gtt cca aag gag acg gct ctg tga cgacctctgg gtgggttggg 1395
 Arg Val Pro Lys Glu Thr Ala Leu
 280 285

gggatatccaa gggagggttg ctcggagctt cacggcacct tggcttcct tctctggaaa 1455

aggaatcctg gttaacaccc cgacagtgcc tggagcttgt atcccaagtc ttccacctgg 1515

acatgctgtg tagacccttg aatcatgaac cctccatctc caaacctgtt ctteggtttt 1575

cgagtgcgcc agatgaccct ggaagaacat ctaagctttc tgtccaagac ccctacccaa 1635

catgggacta gcctttgaat tctggagttg tacatgaaat cagtattcgt gaaaaagctt 1695

Gly Ala Tyr Gly Ala Val Cys Ser Ala Val Asp Ser Arg Thr Gly Asn

40

45

50

aag gtg gcc atc aag aag ttg tac cgg ccc ttc cag tcg gag ctg ttt 368

Lys Val Ala Ile Lys Lys Leu Tyr Arg Pro Phe Gln Ser Glu Leu Phe

55

60

65

gcc aag cgc gcc tac aga gag ttg cgc ctc ctc aaa cac atg cgc cac 416

Ala Lys Arg Ala Tyr Arg Glu Leu Arg Leu Leu Lys His Met Arg His

70

75

80

gag aac gtc att ggg cta ctg gat gtg ttc aca cct gat gag tct ctg 464

Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Asp Glu Ser Leu

85

90

95

gac gac ttc aca gac ttc tac ctg gtg atg cca ttc atg ggc act gat 512

Asp Asp Phe Thr Asp Phe Tyr Leu Val Met Pro Phe Met Gly Thr Asp

100

105

110

115

ctg ggc aaa ctc atg aag cat gag acc ctg agt gaa gac aga atc cag 560

Leu Gly Lys Leu Met Lys His Glu Thr Leu Ser Glu Asp Arg Ile Gln

120

125

130

ttt ctt gtg tat cag atg ttg aag ggg ctg aag tat atc cat gcg gct 608

Phe Leu Val Tyr Gln Met Leu Lys Gly Leu Lys Tyr Ile His Ala Ala

135

140

145

ggg gtc atc cac aga gac ttg aag cct ggc aac ctg gct gtg aat gag 656

Gly Val Ile His Arg Asp Leu Lys Pro Gly Asn Leu Ala Val Asn Glu

150

155

160

gac tgt gag ctg aag atc cta gac ttt ggc ctt gcc agg cag gca gac 704

Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Gln Ala Asp

165

170

175

agt gag atg aca gga tat gtg gta acc cgg tgg tat cgg gca cca gag 752

Ser Glu Met Thr Gly Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu

180

185

190

195

gtc atc ttg aat tgg atg cgc tac acg cag aca gtg gac att tgg tcc	800
Val Ile Leu Asn Trp Met Arg Tyr Thr Gln Thr Val Asp Ile Trp Ser	
200 205 210	
gtt ggc tgc atc atg gcg gag atg att act ggg aag atc ctg ttc aaa	848
Val Gly Cys Ile Met Ala Glu Met Ile Thr Gly Lys Ile Leu Phe Lys	
215 220 225	
ggc aat gac cac ctg gac cag ctg aag gag atc atg aag atc aca ggg	896
Gly Asn Asp His Leu Asp Gln Leu Lys Glu Ile Met Lys Ile Thr Gly	
230 235 240	
acg ccc cct cct gag ttt gtt cag aag cta cag agt gca gag gcc aag	944
Thr Pro Pro Pro Glu Phe Val Gln Lys Leu Gln Ser Ala Glu Ala Lys	
245 250 255	
aac tac atg gaa ggc ctc cct gag tta gaa aag aag gat ttt gcc tct	992
Asn Tyr Met Glu Gly Leu Pro Glu Leu Glu Lys Lys Asp Phe Ala Ser	
260 265 270 275	
gtc ctg acc aac gca agc cct cag gct gtg aat ctc ctg gaa agg atg	1040
Val Leu Thr Asn Ala Ser Pro Gln Ala Val Asn Leu Leu Glu Arg Met	
280 285 290	
ctg gtg ctg gat gcg gaa cag cgg gtg aca gca gct gag gcg tta acc	1088
Leu Val Leu Asp Ala Glu Gln Arg Val Thr Ala Ala Glu Ala Leu Thr	
295 300 305	
cat cca tac ttt gag tcc ctt cgg gac act gag gat gaa ccc aag gcc	1136
His Pro Tyr Phe Glu Ser Leu Arg Asp Thr Glu Asp Glu Pro Lys Ala	
310 315 320	
cag aaa tat gac gac tcc ttt gat gat gta gac cgc acc ctt gag gaa	1184
Gln Lys Tyr Asp Asp Ser Phe Asp Asp Val Asp Arg Thr Leu Glu Glu	
325 330 335	
tgg aag cgt gtg act tac aag gaa gtt ctc agc ttc aag cct cct agg	1232

Trp Lys Arg Val Thr Tyr Lys Glu Val Leu Ser Phe Lys Pro Pro Arg
 340 345 350 355

cag cta gga gcc aga gtt cca aag gag acg gct ctg tga cgacctctgg 1281
 Gln Leu Gly Ala Arg Val Pro Lys Glu Thr Ala Leu
 360 365

gtgggtttggg gggatatccaa aggaggttgg ctggagctt cacggcacct tggcttccct 1341
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 ttccacctgg acatgctgtg tagacccttg aatcatgaac cctccatctc caaacctgtt 1461
 cttcggcttt cgagtgcgcc agatgaccct ggaagaacat ctaagctttc tgtccaagac 1521
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<210> 74

<211> 768

<212> DNA

<213> M. musculus

<220>

<400> 74

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 agagcccgca aaggaaaatc tcagaggcgg gcaggcgggt agccggcgcg gagtacgccc 120
 tgccacgcag tgaccggggg cgcgcggggc gagcccctga tcccgggtcc ggtcctgggg 180
 cgcggtgctc cggctgggga tgagctcccc gccaccgcc cgcaagggtt tttaccgcca 240
 ggaggtgacc aaaacggcct gggaggtgcg cgccgtgtac caagacctgc agcccgttgg 300
 ctctggtgcc tatggtgcag tgtgctctgc agtagacagc cgcactggca acaagggtggc 360

catcaagaag ttgtaccggc ccttcacgac ggagctgttt gccaaagcgcg cctacagaga 420
gttgcgcctc ctcaaacaca tgcgccacga gaacgtcatt gggctactgg atgtgttcac 480
acctgatgag tctctggacg acttcacaga cttctacctg gtgatgccat tcatgggcac 540
tgatctgggc aaactcatga agcatgagac cctgagtga gacagaatcc agtttcttgt 600
gtatcagatg ttgaaggggc tgaagtatat ccatgcggct ggtgtcatcc acagaatcct 660
agactttggc cttgccaggc aggcagacag tgagatgaca ggatatgtgg taaccocggtg 720
gtatcgggca cagaggtcat cttgaattgg gatgcgctac acgcagac 768

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<211> 866

<212> DNA

<213> M. musculus

<220>

<221> unsure

<222> 727

<223> unknown

<223>

<400> 75

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tgatcccggtg tccggtcctg gggcgcggtg ctccggtctg ggatgagctc cccgccaccc 180
gcccgcgaagg gctttttaccg ccaggagggtg accaaaacgg cctgggagggt gcgcgcogtg 240
taccaagacc tgcagcccggt tggctctggt gcctatggtg cagtgtgctc tgcagtagac 300

agccgcactg gcaacaaggt ggccatcaag aagttgtacc ggcccttcca gtcggagctg 360
tttgccaagc gcgcctacag agagttgcgc ctccctcaaac acatgcgcca cgagaacgtc 420
attgggctac tggatgtgtt cacacctgat gagtctctgg acgacttcac agactttgga 480
catttggtcc gttggctgca tcatggcgga gatgattact gggaagatcc tgttcaaagg 540
caatgaccac ctggaccagc tgaaggagat catgaagatc acagggacgc ccctcctga 600
gtttgttcag aagctacaga gtgcagaggc caagaactac atggaaggcc tccctgagtt 660
agaaaagaag gattttgcct ctgtcctgac ccaacgcagc ccctcaggct gtgaaatctc 720
ctggaanagg atgcctggtg ctcgatgagc gaaacagcgg ggtgaccagc agctgaaggc 780
gttaaccctt ccctacctt tggagttccc cttegggaaa cactggaggg attgaaaccc 840
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<210> 76

<211> 1445

<212> DNA

<213> M. musculus

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<221> CDS

<222> (643)... (876)

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cactgatggg acttctcagt ggacatttgg tccgttggct gcatcatggc ggagatgatt 180
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 ttcggccaag atgtgggtgc tgggtgggccc cccctctgtc cctgcattgt attcctgacc 300
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 agtttgttca gaagctacag agtgcagagg tcagtgggag tgggtggtgg gctggacttg 420
 ggcttggggg ctggcctatc accctttttt ccctcacagg ccaagaacta catggaaggc 480
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 accgctggat ggggtgaagg tctcagggtg ctgggtgagt atgtcccctc ctgtggcttg 600
 gcctgaattg ctcttccac agctgtgaat ctctggaaa gg atg ctg gtg ctg 654
 Met Leu Val Leu
 1
 gat gcg gaa cag cgg gtg aca gca gct gag gcg tta acc cat cca tac 702
 Asp Ala Glu Gln Arg Val Thr Ala Ala Glu Ala Leu Thr His Pro Tyr
 5 10 15 20
 ttt gag tcc ctt cgg gac act gag gat gaa ccc aag gcc cag aaa tat 750
 Phe Glu Ser Leu Arg Asp Thr Glu Asp Glu Pro Lys Ala Gln Lys Tyr
 25 30 35
 gac gac tcc ttt gat gat gta gac cgc acc ctt gag gaa tgg aag cgt 798
 Asp Asp Ser Phe Asp Asp Val Asp Arg Thr Leu Glu Glu Trp Lys Arg
 40 45 50
 gtg act tac aag gaa gtt ctc agc ttc aag cct cct agg cag cta gga 846
 Val Thr Tyr Lys Glu Val Leu Ser Phe Lys Pro Pro Arg Gln Leu Gly
 55 60 65
 gcc aga gtt cca aag gag acg gct ctg tga cgacctctgg gtgggttggg 896
 Ala Arg Val Pro Lys Glu Thr Ala Leu

70

75

gggtatccaa aggaggttgg ctcgagctt cacggcacct tggcttccct tctctggaaa 956
aggaatcctg gttaacaccc cgacagtgcc tggagcttgt atcccaagtc ttccacctgg 1016
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atcatctctt ctggaagtgg gtggattctc ttacaccctt agcctggaat tcgaaccagc 1376
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aaaaaaaaa 1445

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<211> 581

<212> DNA

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<400> 77

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caagtcttcc acctggacat gctgtgtaga cccttgaatc atgaaccctc catctccaaa 180
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caagaccct acccaacatg ggactagcct ttgaattctg gagttgtaca tgaaatcagt 300
attcgtgaaa aagcttcaga gtgagcagag cttaggagac aagtgccaga cctgagctct 360
gctcgtcttg gacaatgcc aaggccaactc ctgagacgga atgagacaga ggttagggga 420
cactgactca gggacatcat ctcttctgga agtgggtgga ttctcttaca cccttagcct 480
ggaattcgaa ccagccattg gtgtagccta agtggctggg ggctaataaa acctacagta 540
gatctccaat aaatatcaaa aatataattt acaaactaat c 581

<210> 78

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 78

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24

<210> 79

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 79

ccaggtggaa gacttgggat ac

22

<210> 80

<211> 21

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<223> PCR Probe

<400> 80

caccccgaca gtgcctggag c

21

<210> 81

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<223> PCR Primer

<400> 81

ggcaaattca acggcacagt

20

<210> 82

<211> 20

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<223> PCR Primer

<400> 82

gggtctcgct cctggaagat

20

<210> 83

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> PCR Probe

<400> 83

aaggccgaga atgggaagct tgtcatc

27

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tcattctcact gtctgcctgc

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<210> 86

<211> 20

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<223> Antisense Oligonucleotide

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<210> 87

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 87

gtaaaagccc ttgcgggcgg

20

<210> 88

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 88

tggcggtaaa agcccttgcg

20

<210> 89

<211> 20

<212> DNA

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20

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 91

aggccgtttt ggtcacctcc.

20

<210> 92

<211> 20

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<223> Antisense Oligonucleotide

<400> 92

cgcacctccc aggccgtttt

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<210> 93

<211> 20

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<223> Antisense Oligonucleotide

<400> 93

gagccaacgg gctgcaggtc

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<210> 94

<211> 20

<212> DNA

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<400> 94

caccagagcc aacgggctgc

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<210> 95

<211> 20

<212> DNA

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<223> Antisense Oligonucleotide

<400> 95

gcaccatagg caccagagcc

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<210> 96

<211> 20

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<223> Antisense Oligonucleotide

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acactgcacc ataggcacca

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<210> 97

<211> 20

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tgagagcac actgcacat

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<210> 99

<211> 20

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agtgcggctg tctactgcag

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<210> 100

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<400> 102

ggccaccttg ttgccagtgc

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<210> 103

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<212> DNA

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<223> Antisense Oligonucleotide

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<210> 104

<211> 20

<212> DNA

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<223> Antisense Oligonucleotide

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<210> 105

<211> 20

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<223> Antisense Oligonucleotide

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gaggaggcgc aactctctgt

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<210> 106

<211> 20

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<223> Antisense Oligonucleotide

<400> 106

tgtgtttgag gaggcgcaac

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<210> 109

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<400> 109

tcaccaggta gaagtctgtg

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<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 110

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<210> 111

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

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<211> 20

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<213> Artificial Sequence

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<400> 113

gaaactggat tctgtcttca

20

<210> 114

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 114

cacaagaaac tggattctgt

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<210> 115

<211> 20

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<400> 115

tgatacacaa gaaactggat

20

<210> 116

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 116

gcctgcctgg caaggccaaa

20

<210> 117

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 117

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<210> 118

<211> 20

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<210> 119

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<400> 119

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20

<210> 120

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 120

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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

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<210> 122

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

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<210> 123

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 123

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20

<210> 124

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 124

ccttcagctg gtccaggtgg

20

<210> 125

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 125

tgatctcctt cagctggtcc

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<210> 126

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 126

cttcatgatc tccttcagct

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<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 127

tccatgtagt tcttggcctc

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<210> 128

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 128

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<210> 129

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 129

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<210> 130

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 130

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<210> 131

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 131

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<210> 132

<211> 20

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<220>

<223> Antisense Oligonucleotide

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<211> 20

<212> DNA

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<223> Antisense Oligonucleotide

<400> 134

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<210> 135

<211> 20

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<220>

<223> Antisense Oligonucleotide

<400> 135

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<210> 136

<211> 20

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<213> Artificial Sequence

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<223> Antisense Oligonucleotide

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<210> 137

<211> 20

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<213> Artificial Sequence

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